4. The method of claim 1, wherein the sequencing step (e) is paired-end sequencing, and wherein the method comprises analyzing the paired-end read to determine the allele of a sequence variation that is linked to the STR.

5. The method of claim 1, wherein step (d) is done on a solid support.

6. The method of claim 1, wherein step (d) is done in solution.

7. The method of claim 1, wherein the method comprises pooling the products of step (a), (b), (c) or (d).

8. The method of claim 1, further comprising analyzing the numbers of STR repeats in further sequence reads of step (e).

9. The method of claim 8, wherein the numbers of STR repeats in the further sequence reads are validated as being accurate only if the further sequence reads match sequence reads from the other strand.

10. The method of claim 8, further comprising determining whether the individual is homozygous for a particular allele of the STR.

11. The method of claim 8, further comprising determining whether the individual is heterozygous for different alleles of the STR.

12. The method of claim 1, wherein the method comprises analyzing a plurality of STRs, thereby producing an STR fingerprint.

13. The method of claim 12, further comprising comparing the STR fingerprint to an STR fingerprint from a second individual to determine if the individuals are related.

14. The method of claim 12, further comprising comparing the STR fingerprint to an STR fingerprint obtained from a sample obtained from a crime scene.

15. The method of claim 12, wherein the genomic sample is from a cancer biopsy.

16. The method of claim 15, further comprising comparing the STR fingerprint for the cancer biopsy to an STR fingerprint for a second cancer biopsy, to provide a clonal analysis of cancer progression.

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